

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Snutch, Terry P.
Baillie, David L.
- (ii) TITLE OF INVENTION: Novel Human Calcium Channels and Related Probes, Cell Lines and Methods
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Oppedahl & Larson
- (B) STREET: 1992 Commerce Street Suite 309
- (C) CITY: Yorktown
- (D) STATE: NY
- (E) COUNTRY: USA
- (F) ZIP: 10598
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: MS DOS 6.0
- (D) SOFTWARE: WordPerfect
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Larson, Marina T.
- (B) REGISTRATION NUMBER: 32038
- (C) REFERENCE/DOCKET NUMBER: NMED.P-001-US
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (914) 245-3252
- (B) TELEFAX: (914) 962-4330

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: rat

(ix) FEATURE: oligonucleotide probe for locating calcium channel genes

(xi)SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCAAAACTC AGGCCTTCTA CTGG 24

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii)MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: rat

(ix) FEATURE: oligonucleotide probe for locating calcium channel genes

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 2:

AACGTGTTCT TGGCTATCGC GGTG 24

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii)MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: rat

(ix) FEATURE: oligonucleotide probe for locating calcium channel genes

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GTGAAAGCAC AGAGCTTCTA CTGG 24

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
(A) ORGANISM: rat
(ix) FEATURE: oligonucleotide probe for locating calcium channel genes
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
AACGTTTCT TGGCCATTGC TGTG 24

(2) INFORMATION FOR SEQ ID NO: 5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
(A) ORGANISM: rat
(ix) FEATURE: oligonucleotide probe for locating calcium channel genes
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
GTAAATCCA ACGTCTTCTA CTGG 28

(2) INFORMATION FOR SEQ ID NO: 6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
(A) ORGANISM: rat
(ix) FEATURE: oligonucleotide probe for locating calcium channel genes
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
AATGTGTTCT TGGCCATTGC GGTG 24

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: rat

(ix) FEATURE: oligonucleotide probe for locating calcium channel genes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTGAAGTCTG TCACGTTT TA CTGG 24

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: rat

(ix) FEATURE: oligonucleotide probe for locating calcium channel genes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

AAGCTCTTCT TGGCCATTGC TGTA 24

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: rat

(ix) FEATURE: oligonucleotide probe for locating calcium channel genes

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GTCAAGTCGC AAGTGTTCTA CTGG 24

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii)MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: rat

(ix) FEATURE: oligonucleotide probe for locating calcium channel genes

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AATGTATTCT TGGCTATCGC TGTG 24

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii)MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: rat

(ix) FEATURE: oligonucleotide probe for locating calcium channel genes

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATCTAYGCYR TSATYGGSAT G 21

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii)MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: rat

(ix) FEATURE: oligonucleotide probe for locating calcium channel genes

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 12:

ATGGACAAYT TYGASTAYTC 20

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii)MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE: expressed sequence tag H55225

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GTGATCACTC	TGGAAGGCTG	GGTGGAGATC	ATGTACTACG	TGATGGATGC	TCACTCCTTC	60
TACAACCTCA	TCTACTTCAT	CCTGCTTATC	ATACCCCTCT	TGCCTTGCAC	CCCATATGGT	120
CTTCCCAGAG	TGAGCTCATC	CACCTCGTCA	TGCCTGACTC	GACGTTCA		168

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii)MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE: expressed sequence tag H55617

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GATGGTCGAG	TACTCCCTGG	ACCTTCAGAA	CATCAACCTG	TCAGCCATCC	GCACCGTGCG	60
CGTCCTGAGG	CCCCTCAAAG	CCATCAACCG	CGTGCCCA			98

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE: expressed sequence tag H55223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CATGCTGGTG	ATCCTGCTGA	ACTGCGTGAC	ACTTGGCATG	TACCAGCCGT	GCGACGACAT	60
GGACTGCCTG	TCCGACCGCT	GCAAGATCCT	GCAG			94

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE: expressed sequence tag H55544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GTATCTCTGG	TTACTTTAGT	AGCCAACACT	CTTGGCTACT	CAGACCTTGG	TCCCATTTAAA	60
TCCCTGCGAA	CCTTGAGAGC	ACTAAGACCT	CTAAGAGCTT	TGTCTAGATT	TGAAGGAATG	120
AGG						123

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE: expressed sequence tag F07776

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TTCTCTCCAT	TGTAGGAATG	TTTCTGGCTG	AACTGATAGA	AAAGTATTTT	GTGTGCCCTA	60
CCCTGTTNCG	AGTGATCCGT	CTTGCCAGGA	TTGGCCGAAT	CCTACGTCTG	ATCAAAGGAG	120
CAAAGGGGAT	CCGCACGCTG	CTCTTTGCTT	TGATGATGTC	CCTTCCTGCG	TTGTTTAACA	180
TCGGNCTCCT	TCTTTTCCTG	GTCATGTTCA	TCTACGNCAT	CTTTGGGATG	TCCAATTTTG	240
CCTATGTTAA	GAGGGAAGTT	GGGATCGATG	ACATGTTNAN	CTTTGAGACC	TTTGGAACA	300
GCATGATCTG	CCTGTTCCAA	ATTACAACCT	CTGCTGGCTG	GGA		343

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5562

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii)MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(ix) FEATURE: human alpha-I partial sequence from BAC bK206c7

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 18:

ATG TTT TTC GTC TCA GCC AAT CCC TGG GTG AGT TTC ACC AGT TTT GAT TTA AAC	54
Met Phe Phe Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp Leu Asn	
GTG GCC AAT ATG GAC AAC TTC TTC GCC CCC GTT TTC ACC ATG GGC AAA TAT TAT	108
Val Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met Gly Lys Tyr Tyr	
ACG CAA GGC GAC AAG GTG CTG ATG CCG CTG GCG ATT CAG GCT CTG AAA CAG CTG	162
Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile Gln Ala Leu Lys Gln Leu	
ATG TTC AAA TTG GTG GCC ACT GTT GCT CGA ACA CAT GCT ACA CCG TCA CAC ATC	206
Met Phe Lys Leu Val Ala Thr Val Ala Arg Thr His Ala Thr Pro Ser His Ile	
ACG GGT GGT CCT GGA ACA GGG ATG CAC ACG GGC ACC TTC CAG GAA GGA GCT GAG	270
Thr Gly Gly Pro Gly Thr Gly Met His Thr Gly Thr Phe Gln Glu Gly Ala Glu	
CCT GGT TCA TCT CAG CAC CCT GAG GCA CAG GCC ACG TAT ACA GCA GGG TGC ACC	324
Pro Gly Ser Ser Gln His Pro Glu Ala Gln Ala Thr Tyr Thr Ala Gly Cys Thr	

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CCA	GCC	CCC	ACG	GGC	GAT	CCC	ACC	TGC	TGC	TTT	GTC	CTT	GAC	TTG	GTG	TGC	ACG	378
Pro	Ala	Pro	Thr	Gly	Asp	Pro	Thr	Cys	Cys	Phe	Val	Leu	Asp	Leu	Val	Cys	Thr	
TGG	TTT	GAA	TGT	GTC	AGC	ATG	CTG	GTG	ATC	CTG	CTG	AAC	TGC	GTG	ACA	CTT	GGC	432
Trp	Phe	Glu	Cys	Val	Ser	Met	Leu	Val	Ile	Leu	Leu	Asn	Cys	Val	Thr	Leu	Gly	
ATG	TAC	CAG	CCG	TGC	GAC	GAC	ATG	GAC	TGC	CTG	TCC	GAC	CGC	TGC	AAG	ATC	CTG	486
Met	Tyr	Gln	Pro	Cys	Asp	Asp	Met	Asp	Cys	Leu	Ser	Asp	Arg	Cys	Lys	Ile	Leu	
CAG	GTC	TTT	GAT	GAC	TTC	ATC	TTT	ATC	TTC	TTT	GCC	ATG	GAG	ATG	GTG	CTC	AAG	540
Gln	Val	Phe	Asp	Asp	Phe	Ile	Phe	Ile	Phe	Phe	Ala	Met	Glu	Met	Val	Leu	Lys	
ATG	GTG	GCC	CTG	GGG	ATT	TTT	GGC	AAG	AAG	TGC	TAC	CTC	GGG	GAC	ACA	TGG	AAC	594
Met	Val	Ala	Leu	Gly	Ile	Phe	Gly	Lys	Lys	Cys	Tyr	Leu	Gly	Asp	Thr	Trp	Asn	
CGC	CTG	GAT	TTC	TTC	ATC	GTC	ATG	GCA	GGC	AAC	ATC	AAC	CTG	TCA	GCC	ATC	CGC	648
Arg	Leu	Asp	Phe	Phe	Ile	Val	Met	Ala	Gly	Asn	Ile	Asn	Leu	Ser	Ala	Ile	Arg	
ACC	GTG	CGC	GTC	CTG	AGG	CCC	CTC	AAA	GCC	ATC	AAC	CGC	GTG	CCC	AGT	ATG	CGG	702
Thr	Val	Arg	Val	Leu	Arg	Pro	Leu	Lys	Ala	Ile	Asn	Arg	Val	Pro	Ser	Met	Arg	
ATC	CTG	GTG	AAC	CTG	CTC	CTG	GAC	ACA	CTG	CCC	ATG	CTG	GGG	AAT	GTC	CTG	CTG	756
Ile	Leu	Val	Asn	Leu	Leu	Leu	Asp	Thr	Leu	Pro	Met	Leu	Gly	Asn	Val	Leu	Leu	
CTC	TGC	TTC	TTT	GTC	TTC	TTC	ATC	TTT	GGC	ATC	ATA	GGT	GTG	CAG	CTC	TGG	GCG	810
Leu	Cys	Phe	Phe	Val	Phe	Phe	Ile	Phe	Gly	Ile	Ile	Gly	Val	Gln	Leu	Trp	Ala	
GGC	CTG	CTG	CGT	AAC	CGC	TGC	TTC	CTG	GAG	GAG	AAC	TTC	ACC	ATA	CAA	GGG	GAT	864
Gly	Leu	Leu	Arg	Asn	Arg	Cys	Phe	Leu	Glu	Glu	Asn	Phe	Thr	Ile	Gln	Gly	Asp	
GTG	GCC	TTG	CCC	CCA	TAC	TAC	CAG	CCG	GAG	GAG	GAT	GAT	GAG	ATG	CCC	TTC	ATC	918
Val	Ala	Leu	Pro	Pro	Tyr	Tyr	Gln	Pro	Glu	Glu	Asp	Asp	Glu	Met	Pro	Phe	Ile	
TGC	TCC	CTG	TCG	GGC	GAC	AAT	GGG	ATA	ATG	GGC	TGC	CAT	GAG	ATC	CCC	CCG	CTC	972
Cys	Ser	Leu	Ser	Gly	Asp	Asn	Gly	Ile	Met	Gly	Cys	His	Glu	Ile	Pro	Pro	Leu	
AAG	GAG	CAG	GGC	CGT	GAG	TGC	TGC	CTG	TCC	AAG	GAC	GAC	GTC	TAC	GAC	TTT	GGG	1026
Lys	Glu	Gln	Gly	Arg	Glu	Cys	Cys	Leu	Ser	Lys	Asp	Asp	Val	Tyr	Asp	Phe	Gly	
GCG	GGG	CGC	CAG	GAC	CTC	AAT	GCC	AGC	GGC	CTC	TGT	GTC	AAC	TGG	AAC	CGT	TAC	1080
Ala	Gly	Arg	Gln	Asp	Leu	Asn	Ala	Ser	Gly	Leu	Cys	Val	Asn	Trp	Asn	Arg	Tyr	

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TAC	AAT	GTG	TGC	CGC	ACG	GGC	AGC	GCC	AAC	CCC	CAC	AAG	GGT	GCC	ATC	AAC	TTT	1134
Tyr	Asn	Val	Cys	Arg	Thr	Gly	Ser	Ala	Asn	Pro	His	Lys	Gly	Ala	Ile	Asn	Phe	
GAC	AAC	ATC	GGT	TAT	GCT	TGG	ATT	GTC	ATC	TTC	CAG	GTG	ATC	ACT	CTG	GAA	GGC	1188
Asp	Asn	Ile	Gly	Tyr	Ala	Trp	Ile	Val	Ile	Phe	Gln	Val	Ile	Thr	Leu	Glu	Gly	
TGG	GTG	GAG	ATC	ATG	TAC	TAC	GTG	ATG	GAT	GCT	CAC	TCC	TTC	TAC	AAC	TTC	ATC	1242
Trp	Val	Glu	Ile	Met	Tyr	Tyr	Val	Met	Asp	Ala	His	Ser	Phe	Tyr	Asn	Phe	Ile	
TAC	TTC	ATC	CTG	CTT	ATC	ATA	AGT	GAG	CTC	ATC	CAC	CTC	GTC	ATG	CCT	GAC	TGC	1296
Tyr	Phe	Ile	Leu	Leu	Ile	Ile	Ser	Glu	Leu	Ile	His	Leu	Val	Met	Pro	Asp	Cys	
AGC	TTC	AGC	ACA	GCA	CAG	TCC	CCA	AAA	TGT	CAA	GGT	GAT	TCA	CTC	CCA	GGA	GTC	1350
Ser	Phe	Ser	Thr	Ala	Gln	Ser	Pro	Lys	Cys	Gln	Gly	Asp	Ser	Leu	Pro	Gly	Val	
GCT	GCT	GAA	TCC	CTG	CTG	CTG	CGA	GAC	TCT	AGC	TCC	TCA	GTC	ATC	ACT	GAT	GAG	1404
Ala	Ala	Glu	Ser	Leu	Leu	Leu	Arg	Asp	Ser	Ser	Ser	Ser	Val	Ile	Thr	Asp	Glu	
GCT	GCA	GCC	ATG	GAG	AAC	CTC	CTG	GCG	GGC	ACC	TCC	AAG	GGG	GAT	GAA	AGC	TAT	1458
Ala	Ala	Ala	Met	Glu	Asn	Leu	Leu	Ala	Gly	Thr	Ser	Lys	Gly	Asp	Glu	Ser	Tyr	
CTG	CTC	AGG	CTG	GCC	GGC	AGC	CAA	GTT	CAC	TCC	CAG	GCT	CAG	CAA	ATG	CTG	GGG	1512
Leu	Leu	Arg	Leu	Ala	Gly	Ser	Gln	Val	His	Ser	Gln	Ala	Gln	Gln	Met	Leu	Gly	
AGG	GGG	CTG	GGC	CCT	GAA	AGC	CTG	GAA	ACT	GGA	GAG	GAG	CCC	CAC	TCG	TGG	AGC	1566
Arg	Gly	Leu	Gly	Pro	Glu	Ser	Leu	Glu	Thr	Gly	Glu	Glu	Pro	His	Ser	Trp	Ser	
CCT	CGG	GCC	ACA	AGG	AGA	TGG	GAT	CCC	CAA	TGC	CAA	CCA	GGG	CAG	CCT	CTC	CCC	1620
Pro	Arg	Ala	Thr	Arg	Arg	Trp	Asp	Pro	Gln	Cys	Gln	Pro	Gly	Gln	Pro	Leu	Pro	
CTT	CAT	TTC	ATG	CAA	GCA	CAG	GTG	GGC	TCC	TTC	TTC	ATG	ATC	AAC	CTG	TGC	CTC	1674
Leu	His	Phe	Met	Gln	Ala	Gln	Val	Gly	Ser	Phe	Phe	Met	Ile	Asn	Leu	Cys	Leu	
GTT	GTC	ATA	GCG	ACC	CAG	TTC	TCG	GAG	ACC	AAG	CAA	CGG	GAG	CAC	CGG	CTG	ATG	1728
Val	Val	Ile	Ala	Thr	Gln	Phe	Ser	Glu	Thr	Lys	Gln	Arg	Glu	His	Arg	Leu	Met	
CTG	GAG	CAG	CGG	CAG	CGC	TAC	CTG	TCC	TCC	AGC	ACG	GTG	GCC	AGC	TAC	GCC	GAG	1782
Leu	Glu	Gln	Arg	Gln	Arg	Tyr	Leu	Ser	Ser	Ser	Thr	Val	Ala	Ser	Tyr	Ala	Glu	
CCT	GGC	GAC	TGC	TAC	GAG	GAG	ATC	TTC	CAG	TAT	GTC	TGC	CAC	ATC	CTG	CGC	AAG	1836
Pro	Gly	Asp	Cys	Tyr	Glu	Glu	Ile	Phe	Gln	Tyr	Val	Cys	His	Ile	Leu	Arg	Lys	

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GCC AAG CGC CGC GCC CTG GGC CTC TAC CAG GCC CTG CAG AGC CGG CGC CAG GCC	1890
Ala Lys Arg Arg Ala Leu Gly Leu Tyr Gln Ala Leu Gln Ser Arg Arg Gln Ala	
CTG GGC CCG GAG GCC CCG GCC CCC GCC AAA CCT GGG CCC CAC GCC AAG GAG CCC	1944
Leu Gly Pro Glu Ala Pro Ala Pro Ala Lys Pro Gly Pro His Ala Lys Glu Pro	
CGG CAC TAC CCT CTC ACA GTC TGG GAA TCG ATT CTT GGG AGG CAA GCA GAA GAA	1998
Arg His Tyr Pro Leu Thr Val Trp Glu Ser Ile Leu Gly Arg Gln Ala Glu Glu	
TGC ACG CTC AGA GCT GCC GCC CAC CCG TCC TCG GGT GCC AGC CAT CCA GGC GTG	2049
Cys Thr Leu Arg Ala Ala Ala His Pro Ser Ser Gly Ala Ser His Pro Gly Val	
GGC TCG GAG GAG GCC CCA GAG CTG TGC CCG CAA CAT AGC CCC CTG GAT GCG ACG	2106
Gly Ser Glu Glu Ala Pro Glu Leu Cys Pro Gln His Ser Pro Leu Asp Ala Thr	
CCC CAC ACC CTG GTG CAG CCC ATC CCC GCC ACG CTG GCT TCC GAT CCC GCC AGC	2160
Pro His Thr Leu Val Gln Pro Ile Pro Ala Thr Leu Ala Ser Asp Pro Ala Ser	
TGC CCT TGC TGC CAG CAT GAG GAC GGC CGG CGG CCC TCG GGC CTG GGC AGC ACC	2214
Cys Pro Cys Cys Gln His Glu Asp Gly Arg Arg Pro Ser Gly Leu Gly Ser Thr	
GAC TCG GGC CAG GAG GGC TCG GGC TCC GGG AGC TCC GCT GGT GGC GAG GAC GAG	2268
Asp Ser Gly Gln Glu Gly Ser Gly Ser Gly Ser Ser Ala Gly Gly Glu Asp Glu	
GCG GAT GGG GAC GGG GCC CGG AGC AGC GAG GAC GGA GCC TCC TCA GAA CTG GGG	2322
Ala Asp Gly Asp Gly Ala Arg Ser Ser Glu Asp Gly Ala Ser Ser Glu Leu Gly	
AAG GAG GAG GAG GAG GAG GAG CAG GCG GAT GGG GCG GTC TGG CTG TGC GGG GAT	2376
Lys Glu Glu Glu Glu Glu Glu Gln Ala Asp Gly Ala Val Trp Leu Cys Gly Asp	
GTG TGG CGG GAG ACG CGA GCC AAG CTG CGC GGC ATC GTG GAC AGC AAG TAC TTC	2430
Val Trp Arg Glu Thr Arg Ala Lys Leu Arg Gly Ile Val Asp Ser Lys Tyr Phe	
AAC CGG GGC ATC ATG ATG GCC ATC CTG GTC AAC ACC GTC AGC ATG GGC ATC GAG	2484
Asn Arg Gly Ile Met Met Ala Ile Leu Val Asn Thr Val Ser Met Gly Ile Glu	
CAC CAC GAG CAG GCC AGT GCA GCG CAG CCG GGC CGG GCC TGC GGG AGA GGA CAA	2538
His His Glu Gln Ala Ser Ala Ala Gln Pro Gly Arg Ala Cys Gly Arg Gly Gln	
AAT CCA GAC CTT TGC ATG ACC CTC AAG GCC CCT TGT CTC TGT CAC AAC GTC CCT	2592
Asn Pro Asp Leu Cys Met Thr Leu Lys Ala Pro Cys Leu Cys His Asn Val Pro	

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TCA	CCA	GGC	CAG	GGT	GTC	CTG	TCC	CAT	CCA	GTG	ACT	CCA	CCC	CAT	ACA	GCC	CCA	2646
Ser	Pro	Gly	Gln	Gly	Val	Leu	Ser	His	Pro	Val	Thr	Pro	Pro	His	Thr	Ala	Pro	
TGG	CGC	ATG	GAG	ACA	GGA	AAG	CAG	GGA	CAC	GGA	TGT	GAA	GAA	GGA	CCA	GGA	CAA	2700
Trp	Arg	Met	Glu	Thr	Gly	Lys	Gln	Gly	His	Gly	Cys	Glu	Glu	Gly	Pro	Gly	Gln	
CGA	AGC	AGT	GAC	ATG	TTT	GCC	CTG	GAG	ATG	ATC	CTG	AAG	CTG	GCT	GCA	TTT	GGG	2754
Arg	Ser	Ser	Asp	Met	Phe	Ala	Leu	Glu	Met	Ile	Leu	Lys	Leu	Ala	Ala	Phe	Gly	
CTC	TTC	GAC	TAC	CTG	CGT	AAC	CCC	TAC	AAC	ATC	TTC	GAC	AGC	ATC	ATT	GTC	ATC	2808
Leu	Phe	Asp	Tyr	Leu	Arg	Asn	Pro	Tyr	Asn	Ile	Phe	Asp	Ser	Ile	Ile	Val	Ile	
ATC	AGC	ATC	TGG	GAG	ATC	GTG	GGG	CAG	GCG	GAC	GGT	GGG	CTG	TCG	GTG	CTG	CGG	2862
Ile	Ser	Ile	Trp	Glu	Ile	Val	Gly	Gln	Ala	Asp	Gly	Gly	Leu	Ser	Val	Leu	Arg	
ACC	TTC	CGG	CTG	CTG	CGC	GTG	CTG	AAA	CTG	GTG	CGC	TTC	ATG	CCT	GCC	CTG	CGG	2916
Thr	Phe	Arg	Leu	Leu	Arg	Val	Leu	Lys	Leu	Val	Arg	Phe	Met	Pro	Ala	Leu	Arg	
CGC	CAG	CTC	GTG	GTG	CTC	ATG	AAG	ACC	ATG	GAC	AAC	GTG	GCC	ACC	TTC	TGC	ATG	2970
Arg	Gln	Leu	Val	Val	Leu	Met	Lys	Thr	Met	Asp	Asn	Val	Ala	Thr	Phe	Cys	Met	
CTG	CTC	ATG	CTC	TTC	ATC	TTC	ATC	TTC	AGC	ATC	CTT	GGG	ATG	CAT	ATT	TTT	GGC	3024
Leu	Leu	Met	Leu	Phe	Ile	Phe	Ile	Phe	Ser	Ile	Leu	Gly	Met	His	Ile	Phe	Gly	
TGC	AAG	TTC	AGC	CTC	CGC	ACG	GAC	ACT	GGA	GAC	ACG	GTG	CCC	GAC	AGG	AAG	AAC	3078
Cys	Lys	Phe	Ser	Leu	Arg	Thr	Asp	Thr	Gly	Asp	Thr	Val	Pro	Asp	Arg	Lys	Asn	
TTC	GAC	TCC	CTG	CTG	TGG	GCC	ATC	GTC	ACT	GTG	TTC	CAG	ATC	CTC	ACC	CAG	GAG	3132
Phe	Asp	Ser	Leu	Leu	Trp	Ala	Ile	Val	Thr	Val	Phe	Gln	Ile	Leu	Thr	Gln	Glu	
GAC	TGG	AAC	GTC	GTT	CTC	TAC	AAT	GGC	ATG	GCC	TCC	ACT	TCT	CCC	TGG	GCC	TCC	3186
Asp	Trp	Asn	Val	Val	Leu	Tyr	Asn	Gly	Met	Ala	Ser	Thr	Ser	Pro	Trp	Ala	Ser	
CTC	TAC	TTT	GTC	GCC	CTC	ATG	ACC	TTC	GGC	AAC	TAT	GTG	CTC	TTC	AAC	CTG	CTG	3240
Leu	Tyr	Phe	Val	Ala	Leu	Met	Thr	Phe	Gly	Asn	Tyr	Val	Leu	Phe	Asn	Leu	Leu	
GTG	GCC	ATC	CTG	GTG	GAG	GGC	TTC	CAG	GCG	GAG	GTG	ACT	GTG	GTC	TTG	GCA	GAG	3294
Val	Ala	Ile	Leu	Val	Glu	Gly	Phe	Gln	Ala	Glu	Val	Thr	Val	Val	Leu	Ala	Glu	
GAA	GCA	CCC	CCA	CAG	GGC	CTG	CGA	AAG	ACT	GGG	CGA	GGG	AGA	GGT	GGC	CTG	GAT	3348
Glu	Ala	Pro	Pro	Gln	Gly	Leu	Arg	Lys	Thr	Gly	Arg	Gly	Arg	Gly	Gly	Leu	Asp	

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GGG GGA GGG CTG CAA TTC AAA CTT CTA GCA GGC AAC CTA TCC CTA AAG GAG GGG	3402
Gly Gly Gly Leu Gln Phe Lys Leu Leu Ala Gly Asn Leu Ser Leu Lys Glu Gly	
GTT GCT GAT GAG GTG GGT GAC GCC AAT CGC TCC TAC TCG GAC GAG GAC CAG AGC	3456
Val Ala Asp Glu Val Gly Asp Ala Asn Arg Ser Tyr Ser Asp Glu Asp Gln Ser	
TCA TCC AAC ATA GAA GAG TTT GAT AAG CTC CAG GAA GGC CTG GAC AGC AGC GGA	3510
Ser Ser Asn Ile Glu Glu Phe Asp Lys Leu Gln Glu Gly Leu Asp Ser Ser Gly	
GAT CCC AAG CTC TGC CCA ATC CCC ATG ACC CCC AAT GGG CAC CTG GAC CCC AGT	3564
Asp Pro Lys Leu Cys Pro Ile Pro Met Thr Pro Asn Gly His Leu Asp Pro Ser	
CTC CCA CTG GGT GGG CAC CTA GGT CCT GCT GGG GCT GCG GGA CCT GCC CCC CGA	3618
Leu Pro Leu Gly Gly His Leu Gly Pro Ala Gly Ala Ala Gly Pro Ala Pro Arg	
CTC TCA CTG CAG CCG GAC CCC ATG CTG GTG GCC CTG GGC TCC CGA AAG AGC AGC	3672
Leu Ser Leu Gln Pro Asp Pro Met Leu Val Ala Leu Gly Ser Arg Lys Ser Ser	
GTC ATG TCT CTA GGG AGG ATG AGC TAT GAC CAG CGC TCC CTG GTG GGT GGT CTT	3726
Val Met Ser Leu Gly Arg Met Ser Tyr Asp Gln Arg Ser Leu Val Gly Gly Leu	
AGA GCC ACA GCG GGG GTG CAG GCT GCC TTT GGG CAC CTG GTG CCC CAG CCG TGG	3780
Arg Ala Thr Ala Gly Val Gln Ala Ala Phe Gly His Leu Val Pro Gln Pro Trp	
GTG TGC CTG TGG GGC GCT GAC CCG AAC GGG AAC TCC TTC CAG TCC AGC TCC CGG	3834
Val Cys Leu Trp Gly Ala Asp Pro Asn Gly Asn Ser Phe Gln Ser Ser Ser Arg	
AGC TCC TAC TAC GGG CCA TGG GGC CGC AGC GCG GCC TGG GCC AGC CGT CGC TCC	3888
Ser Ser Tyr Tyr Gly Pro Trp Gly Arg Ser Ala Ala Trp Ala Ser Arg Arg Ser	
AGC TGG AAC AGC CTC AAG CAC AAG CCG CCG TCG GCG GAG CAT GAG TCC CTG CTC	3942
Ser Trp Asn Ser Leu Lys His Lys Pro Pro Ser Ala Glu His Glu Ser Leu Leu	
TCT GCG GAG CGC GGC GGC GGC GCC CGG GTC TGC GAG GTT GCC GCG GAC GAG GGG	3996
Ser Ala Glu Arg Gly Gly Gly Ala Arg Val Cys Glu Val Ala Ala Asp Glu Gly	
CCG CCG CGG GCC GCA CCC CTG CAC ACC CCA CAC GCC CAC CAC GTT CAT CAC GGG	4050
Pro Pro Arg Ala Ala Pro Leu His Thr Pro His Ala His His Val His His Gly	
CCC CAT CTG GCG CAC CGC CAC CGC CAC CAC CGC CGG ACG CTG TCC CTC GAC AAC	4104
Pro His Leu Ala His Arg His Arg His His Arg Arg Thr Leu Ser Leu Asp Asn	

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AGG	GAC	TCG	GTG	GAC	CTG	GCC	GAG	CTG	GTG	CCC	GCG	GTG	GGC	GCC	CAC	CCC	CGG	4158
Arg	Asp	Ser	Val	Asp	Leu	Ala	Glu	Leu	Val	Pro	Ala	Val	Gly	Ala	His	Pro	Arg	
GCC	GCC	TGG	AGG	GCG	GCA	GGC	CCG	GCC	CCC	GGG	CAT	GAG	GAC	TGC	AAT	GGC	AGG	4212
Ala	Ala	Trp	Arg	Ala	Ala	Gly	Pro	Ala	Pro	Gly	His	Glu	Asp	Cys	Asn	Gly	Arg	
ATG	CCC	AGC	ATC	GCC	AAA	GAC	GTC	TTC	ACC	AAG	ATG	GGC	GAC	CGC	GGG	GAT	CGC	4266
Met	Pro	Ser	Ile	Ala	Lys	Asp	Val	Phe	Thr	Lys	Met	Gly	Asp	Arg	Gly	Asp	Arg	
GGG	GAG	GAT	GAG	GAG	GAA	ATC	GAC	TAC	GTG	AGT	GGG	GGC	GGG	GCC	GAA	GGG	GAC	4320
Gly	Glu	Asp	Glu	Glu	Glu	Ile	Asp	Tyr	Val	Ser	Gly	Gly	Gly	Ala	Glu	Gly	Asp	
CTG	ACC	CTG	TGC	TTC	CGC	GTC	CGC	AAG	ATG	ATC	GAC	GTC	TAT	AAG	CCC	GAC	TGG	4374
Leu	Thr	Leu	Cys	Phe	Arg	Val	Arg	Lys	Met	Ile	Asp	Val	Tyr	Lys	Pro	Asp	Trp	
TGC	GAG	GTC	CGC	GAA	GAC	TGG	TCT	GTC	TAC	CTC	TTC	TCT	CCC	GAG	AAC	AGG	CTC	4428
Cys	Glu	Val	Arg	Glu	Asp	Trp	Ser	Val	Tyr	Leu	Phe	Ser	Pro	Glu	Asn	Arg	Leu	
AGG	GAT	CTG	GGC	TGG	GTA	AGC	CTC	GAG	TGC	CAG	GGA	AAG	GTG	GGT	GAC	CTC	GTG	4482
Arg	Asp	Leu	Gly	Trp	Val	Ser	Leu	Glu	Cys	Gln	Gly	Lys	Val	Gly	Asp	Leu	Val	
GTG	TGG	GTG	TAT	GGT	CAG	AGG	AGG	CAG	CGC	CAG	ACC	ATT	ATT	GCC	CAC	AAA	CTC	4536
Val	Trp	Val	Tyr	Gly	Gln	Arg	Arg	Gln	Arg	Gln	Thr	Ile	Ile	Ala	His	Lys	Leu	
TTC	GAC	TAC	GTC	GTC	CTG	GCC	TTC	ATC	TTT	CTC	AAC	TGC	ATC	ACC	ATC	GCC	CTG	4590
Phe	Asp	Tyr	Val	Val	Leu	Ala	Phe	Ile	Phe	Leu	Asn	Cys	Ile	Thr	Ile	Ala	Leu	
GAG	CGG	CCT	CAG	ATC	GAG	GCC	GGC	AGC	ACC	GAA	CGC	ATC	TTT	CTC	ACC	GTG	TCC	4644
Glu	Arg	Pro	Gln	Ile	Glu	Ala	Gly	Ser	Thr	Glu	Arg	Ile	Phe	Leu	Thr	Val	Ser	
AAC	TAC	ATC	TTC	ACG	GCC	ATC	TTC	GTG	GGC	GAG	ATG	ACA	TTG	AAG	GTA	GTC	TCG	4698
Asn	Tyr	Ile	Phe	Thr	Ala	Ile	Phe	Val	Gly	Glu	Met	Thr	Leu	Lys	Val	Val	Ser	
CTG	GGC	CTG	TAC	TTC	GGC	GAG	CAG	GCG	TAC	CTA	CGC	AGC	AGC	TGG	AAC	GTG	CTG	4752
Leu	Gly	Leu	Tyr	Phe	Gly	Glu	Gln	Ala	Tyr	Leu	Arg	Ser	Ser	Trp	Asn	Val	Leu	
GAT	GGC	TTT	CTT	GTC	TTC	GTG	TCC	ATC	ATC	GAC	ATC	GTG	GTG	TCC	CTG	GCC	TCA	4806
Asp	Gly	Phe	Leu	Val	Phe	Val	Ser	Ile	Ile	Asp	Ile	Val	Val	Ser	Leu	Ala	Ser	
GCC	GGG	GGA	GCC	AAG	ATC	TTG	GGG	GTC	CTC	CGA	GTC	TTG	CGG	CTC	CTG	CGC	ACC	4860
Ala	Gly	Gly	Ala	Lys	Ile	Leu	Gly	Val	Leu	Arg	Val	Leu	Arg	Leu	Leu	Arg	Thr	

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CTA	CGC	CCC	CTG	CGT	GTC	ATC	AGC	CGG	GCG	CCG	GGC	CTG	AAG	CTG	GTG	GTG	GAG	4914
Leu	Arg	Pro	Leu	Arg	Val	Ile	Ser	Arg	Ala	Pro	Gly	Leu	Lys	Leu	Val	Val	Glu	
ACA	CTC	ATC	TCC	TCC	CTC	AAG	CCC	ATC	GGC	AAC	ATC	GTG	CTC	ATC	TGC	TGT	GCC	4968
Thr	Leu	Ile	Ser	Ser	Leu	Lys	Pro	Ile	Gly	Asn	Ile	Val	Leu	Ile	Cys	Cys	Ala	
TTC	TTC	ATC	ATC	TTT	GGC	ATC	CTG	GGA	GTG	CAG	CTC	TTC	AAG	GGC	AAG	TTC	TAC	5022
Phe	Phe	Ile	Ile	Phe	Gly	Ile	Leu	Gly	Val	Gln	Leu	Phe	Lys	Gly	Lys	Phe	Tyr	
CAC	TGT	CTG	GGC	GTG	GAC	ACC	CGC	AAC	ATC	ACC	AAC	CGC	TCG	GAC	TGC	ATG	GCC	5076
His	Cys	Leu	Gly	Val	Asp	Thr	Arg	Asn	Ile	Thr	Asn	Arg	Ser	Asp	Cys	Met	Ala	
GCC	AAC	TAC	CGC	TGG	GTC	CAT	CAC	AAA	TAC	AAC	TTC	GAC	AAC	CTG	GGC	CAG	GCT	5130
Ala	Asn	Tyr	Arg	Trp	Val	His	His	Lys	Tyr	Asn	Phe	Asp	Asn	Leu	Gly	Gln	Ala	
CTG	ATG	TCC	CTC	TTT	GTC	CTG	GCA	TCC	AAG	GAT	GGT	TGG	GTG	AAC	ATC	ATG	TAC	5185
Leu	Met	Ser	Leu	Phe	Val	Leu	Ala	Ser	Lys	Asp	Gly	Trp	Val	Asn	Ile	Met	Tyr	
AAT	GGA	CTG	GAT	GCT	GTT	GCT	GTG	GAC	CAG	CAG	CCT	GTG	ACC	AAC	CAC	AAC	CCC	5238
Asn	Gly	Leu	Asp	Ala	Val	Ala	Val	Asp	Gln	Gln	Pro	Val	Thr	Asn	His	Asn	Pro	
TGG	ATG	CTG	CTG	TAC	TTC	ATC	TCC	TTC	CTG	CTC	ATC	GTC	AGC	TTC	TTT	GTG	CTC	5292
Trp	Met	Leu	Leu	Tyr	Phe	Ile	Ser	Phe	Leu	Leu	Ile	Val	Ser	Phe	Phe	Val	Leu	
AAC	ATG	TTT	GTG	GGT	GTC	GTG	GTG	GAG	AAC	TTC	CAC	AAG	TGC	CGG	CAG	CAC	CAG	5346
Asn	Met	Phe	Val	Gly	Val	Val	Val	Glu	Asn	Phe	His	Lys	Cys	Arg	Gln	His	Gln	
GAG	GCT	GAA	GAG	GCA	CGG	CGG	CGT	GAG	GAG	AAG	CGG	CTG	CGG	CGC	CTG	GAG	AAG	5400
Glu	Ala	Glu	Glu	Ala	Arg	Arg	Arg	Glu	Glu	Lys	Arg	Leu	Arg	Arg	Leu	Glu	Lys	
AAG	CGC	CGG	AAG	GCC	CAG	CGG	CTG	CCC	TAC	TAT	GCC	ACC	TAT	TGT	CAC	ACC	CGG	5454
Lys	Arg	Arg	Lys	Ala	Gln	Arg	Leu	Pro	Tyr	Tyr	Ala	Thr	Tyr	Cys	His	Thr	Arg	
CTG	CTC	ATC	CAC	TCC	ATG	TGC	ACC	AGC	CAC	TAC	CTG	GAC	ATC	TTC	ATC	ACC	TTC	5508
Leu	Leu	Ile	His	Ser	Met	Cys	Thr	Ser	His	Tyr	Leu	Asp	Ile	Phe	Ile	Thr	Phe	
ATC	ATC	TGC	CTC	AAC	GTG	GTC	ACC	ATG	TCC	CTG	GAG	CAC	TAC	AAT	CAG	CCC	ACG	5562
Ile	Ile	Cys	Leu	Asn	Val	Val	Thr	Met	Ser	Leu	Glu	His	Tyr	Asn	Gln	Pro	Thr	

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 567

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
(A) ORGANISM: human
(ix) FEATURE: human alpha-I partial sequence
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATG CGG ATC CTG GTG AAC CTG CTC CTG GAC ACA CTG CCC ATG CTG GGG AAT GTC	54
Met Arg Ile Leu Val Asn Leu Leu Leu Asp Thr Leu Pro Met Leu Gly Asn Val	
CTG CTG CTC TGC TTC TTT GTC TTC TTC ACC TTT GGC ATC ATA GGT GTG CAG CTC	108
Leu Leu Leu Cys Phe Phe Val Phe Phe Thr Phe Gly Ile Ile Gly Val Gln Leu	
TGG GCG GGC CTG CTG CGT AAC CGC TGC TTC CTG GAG GAG AAC TTC ACC ATA CAA	162
Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu Glu Asn Phe Thr Ile Gln	
GGG GAT GTG GCC TTG CCC CCA TAC TAC CAG CCG GAG GAG GAT GAT GAG ATG CCC	216
Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln Pro Glu Glu Asp Asp Glu Met Pro	
TTC ATC TGC TCC CTG TCG GGC GAC AAT GGG ATA ATG GGC TGC CAT GAG ATC CCC	270
Phe Ile Cys Ser Leu Ser Gly Asp Asn Gly Ile Met Gly Cys His Glu Ile Pro	
CCG CTC AAG GAG CAG GGC CGT GAG TGC TGC CTG TCC AAG GAC GAC GTC TAC GAC	324
Pro Leu Lys Glu Gln Gly Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp	
TTT GGG GCG GGG CGC CAG GAC CTC AAT GCC AGC GGC CTC TGT GTC AAC TGG AAC	378
Phe Gly Ala Gly Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn	
CGT TAC TAC AAT GTG TGC CGC ACG GGC AGC GCC AAC CCC CAC AAG GGT GCC ATC	432
Arg Tyr Tyr Asn Val Cys Arg Thr Gly Ser Ala Asn Pro His Lys Gly Ala Ile	
AGC TTT GAC AAC ATC GGT TAT GCT TGG ATT GTC ATC TTC CAG GTG ATC ACT CTG	486
Ser Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln Val Ile Thr Leu	
GAA GGC TGG GTG GCG ATC ATG TAC TAC GTG ATG GAT GCT CTC TCC TTC TAC AAC	540
Glu Gly Trp Val Ala Ile Met Tyr Tyr Val Met Asp Ala Leu Ser Phe Tyr Asn	
TTC GTC TAC TTC ATC CTG CTT ATC ATA	567
Phe Val Tyr Phe Ile Leu Leu Ile Ile	

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(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 567

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: rat

(ix) FEATURE: rat alpha-I partial sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ATG CGG ATC CTG GTG AAC CTG CTG CTC GAC ACG CTG CCC ATG CTG GGG AAC GTG	54
Met Arg Ile Leu Val Asn Leu Leu Leu Asp Thr Leu Pro Met Leu Gly Asn Val	
CTC CTG CTC TGT TTC TTC GTC TTC TTC ATC TTC GGC ATC ATT GGC GTG CAG CTC	108
Leu Leu Leu Cys Phe Phe Val Phe Phe Ile Phe Gly Ile Ile Gly Val Gln Leu	
TGG GCA GGC CTG CTA CGG AAC CGC TGC TTC CTG GAA GAA AAC TTC ACC ATA CAA	162
Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu Glu Asn Phe Thr Ile Gln	
GGG GAT GTG GCC CTG CCC CCT TAT TAC CAA CCA GAG GAG GAT GAC GAG ATG CCC	216
Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln Pro Glu Glu Asp Asp Glu Met Pro	
TTT ATC TGC TCC CTG ACT GGG GAC AAT GGC ATC ATG GGC TGC CAC GAG ATC CCC	270
Phe Ile Cys Ser Leu Thr Gly Asp Asn Gly Ile Met Gly Cys His Glu Ile Pro	
CCA CTG AAG GAG CAG GGC CGG GAA TGC TGC CTG TCC AAA GAT GAT GTG TAT GAC	324
Pro Leu Lys Glu Gln Gly Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp	
TTC GGG GCG GGG CGC CAG GAC CTC AAC GCC AGC GGT CTG TGC GTC AAC TGG AAC	378
Phe Gly Ala Gly Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn	
CGC TAC TAC AAC GTC TGC CGC ACG GGC AAC GCC AAC CCT CAC AAG GGC GCC ATC	432
Arg Tyr Tyr Asn Val Cys Arg Thr Gly Asn Ala Asn Pro His Lys Gly Ala Ile	
AAC TTT GAC AAC ATT GGC TAT GCC TGG ATT GTG ATT TTC CAG GTG ATC ACT CTG	486
Asn Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln Val Ile Thr Leu	

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GAA GGC TGG GTG GAG ATC ATG TAC TAT GTG ATG GAC GCA CAT TCT TTC TAC AAC 540
Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp Ala His Ser Phe Tyr Asn

TTC ATC TAC TTC ATC CTG CTT ATC ATA 567
Phe Ile Tyr Phe Ile Leu Leu Ile Ile

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